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GenCore version 5.1.6
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OM nucleic - nuc	nucleic	search, using sw model	
Run on:	January	<pre>iry 23, 2004, 11:26:23 ; Search time 7464 Seconds (without alignments) 10994.736 Million cell updates/sec</pre>	
Title: Perfect score: Sequence:	US-09 2006 1 gat	US-09-701-572-1 2006 1 gattcggcacgaggaagaaaagaaaaaaaaaaaa	
Scoring table:	IDENT1 Gapop	IDENTITY NUC Gapop 10.0, Gapext 1.0	
Searched:	2888711	711 segs, 20454813386 residues	
Total number of	hits	satisfying chosen parameters: 5777422	
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	37:	em_htg_vrt:*	
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	40:	em_htgo_mus:*	
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Pred. No. is the number of results predicted by chance to have a

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7	86	99	-		AF079404		F079404 Medicago
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n ve	200	ייי מייי	1		AY063875	. ~	Y063875 Arabidops
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on :	72	23			AY099581	4, 1	1Y099581 Arabidops
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RESULT							
LOCUS		AX008931			Ω	DNA linear	ar PAT 06-SEP-2000
DEFINIT		Sequence	1 from	Patent	nt WO9964451.		
ACCESSION VERSION		AX008931.	1 GI:9	9963	28		
KEYWORD			140				
ORGAN		Medicago sati Eukaryota; Vi Spermatophyta	> H	lipla lagno	rept	ophyta; Embryophyta; dicotyledons; core eu	Tracheoph dicots;
		rosids; (Medicago	Ä	÷ H	Fabac	eae;	5

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	acid coding f	CCIENT (FR) Location/Qualifiers 1.2006 /organism="Wedicago sativa" /mol type="qenomic DNA"	/db_xref="taxon:3879" 1821609 /note="unamed protein product" /codon start=1	/proteIn_id="CAC07447.1" /proteIn_id="CAC07447.1" /db_xref="gr1:9956329" /translation="MDGTGNAMPPPTSTVRDNSPPPEPSPESLRHVSRMINSNHYTSP /translation="MDGTGNAMPPPTSGRDDSSSAYTTLLRTALFGPDVAGPVTPER SRTIYSDRFIPSRSASKFALFDINTPTBGRDDSSSAYTTLLRTALFGPDVAGPVTPER	TIDS SAWTI-PINKI TEXTETROSPHELSEPRODDE VPEGVINED VRAKVERSEY KIVL DAPALODDE YLALVDWS SHAVLANGGENCYLEMACSSKYTKL.CDLGVDDCVCSVGWA QROTHLAVGTINNENCYCH TWOARCKKI TRSMEGHRLRVGALAWSSSLLSSGGRDKNI Y QR DIRTQDEDF VSKLSGGHGSEVCGLKWS YDNRELLASGGNDNKLLWWQHSFOYLKYCEBHT DIRTQDEDF VSKLSGGHGSEVCGLKWSY YDNRELLASGGNDNKLCHWQHSFOYLKYCEBHT DAR YDN DE DAR DHT AL A GGGGTRA DHO THE PRAWTTHRINGHI SCHUTGSOYCKII VWSKRYNB	ம	.0%; Score 2006; DB 6; Length 2006; .0%; Pred. No. 0; 0; Mismatches 0; Indels 0; Gaps			CTCCGC CTCCGC	TTCTCC TTCTCC	CAACCA CAACCA	rgcric rgcric	CAGCGC 420 	TACGCC TACGCC	TAAGAC TAAGAC	TCCTGG 	GGTTT 6

Length

us-09-701-572-1.rge

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DB 8;
                       ; Score 1986.4;
; Pred. No. 0;
0; Mismatches
                                                                                       GATTCGGCACGAGGAAGAACAAAGAAACTCTCT
                       99.08;
                             Query Match
Best Local Similarity 99.9
Matches 1987; Conservative
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Medicago sativa subsp. x varia
sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Education (2014)

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A plant cell cycle regulator that controls endoreduplication and cell differentiation

A plant cell cycle regulator that controls endoreduplication and cell differentiation

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protein (At4g22910)

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AY128834.1 GI:22136311

FUL CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.

I (bases 1 to 1541)
SS Trippp, M., Southwick, A., Karlin-Neumann, G., Naguyen, M., Miranda, M.,
Palm, C., U., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission

N. Schinchted (01-JUL-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
Arabidopsis thaliana putative fizzy-related
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/gene="At4g22910"
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PGPETPEKRDITGPSSRNIFRFKTETHRELNSFROGGVENGAGSYVKAPRVV
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SVCSVGWALNGTHANGTGTGYCYQIWDASRCKTRTREGHRLAYGALAMGSSVLSGGS
RDKSILQRDLRCGPBNYSKLAGHKSSVCGLKWSYDNRELASGGONDNRLFWNNQHSTQP
VLKYSEHTAAVKALAMSPHYHGLLASGGGGTADRCIRFWNTTTYTHLSSIDYCSGVCNL
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DETLRFWNNPPSPKSQNQIIVWKYPTMSKIATLTGHTYRVLYLAVSPDGGTIVTGAG
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/note="This clone is in pENTR/SD-dTopo This is a cloned
PCR product using RIKEN clone RAFL09-63-A14 (AY099585) as
a template
ecctype: Columbia"
                                                         The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA: 'RIKEN trabidoplais Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                       The salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAs: Tripp, M., Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tripp,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contribute this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
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e-mail for correspondence: arab@sequence.stanford.edu
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Pred. No. 5.5e-158;
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mRNA

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AY128834

RESULT 3 AY128834 LOCUS

Brank get al

1377 ACTCCCAGAACCAGATTATTGTAGAGATACCCCACTATGTCAAAGCTGGCGACTCTTA 1436	z Σ		Ā	Hayashizaki,Y. and Shinozaki,K. Hayashizaki,Y. and Shinozaki,K. The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.	Nguyen, M, (SSP/Stanford) and Selequally to this work. Shinozak: (SSP/Stanford) contributed equalitiers Location/Qualifiers 1. 1865 / roganism="Arabidopsis/mol_type="mcRNA" / db_xref="rexon:3702" / chromosome="4"	/clone="RAFL09-63-A14 (R24687)" /note="This clone is in pBluescript ecotype: Columbia" 1. 1865 /gene /gene="At4g22910" /note="Bynonym: F7H19.90" CDS 671518
B & B & B & B & B & B & B & B & B & B &	RESULT 4 AY09585 LOCUS DEFINITION ACCESSION VERSION KEYWOORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT		FEATURES	
158 CONSELVATIVE O; MISMATCHES 312; Indels 27; Gaps 4; 158 CONSELVATIVE GAALAATCTACTACTACTACTACTACTACTACTACTACTACTAC	CGGAGACGAGACAGTCCATGCACTTCGCCGTTTATGGATGATGATGTTCTTCCTG CGGAGACTCATCGGTTTTGATTCGTTTTCTTCCTT CGGAGACTCATCGGTCTTTGAATTCGTTTTCTTCCTTTTGGTGTTGATGATTCTCCTG GTGTTAATCATAAGTCCGGTTAAAGCTCCTAGGAAGGTTCCTCGATCGCCTTATAAAG GTGTTTCTCATAGTGGTCCTGTTAAAGCTCCCAGGAAAGTGCCGCGATCGCCGTATAAAG TTTTGGATGGACCTGGTTTGCAAGATGATTTTTATCTGAATCTGGATGGTCTCAC	500 TATIGGAIGCACCGGCCTIGCAAGAIGAIIIIIAICLGAALIIGIGGAIIGGICAGCA 500 717 ACAAIGTGTTGGCTTTGGGTAACTGTGTCTACCTCTGGAATGCTTGTAGCAGCA 776 717 AGGTAACTAAATTATGGAACTAGGGAACTGTGTGTATTTATGGAATGCTTGTAGCAGCA 619 777 AGGTAACTAAATTATGTGATTTGGGGGTTGATGATTGTTTTGTTCTGTTGGGTTGGGCTC 836 620 AGGTTACTAAGTTATGTGATCTCGGAGCATAGTGTTTGTT	837 AACGTGCTACTTTGCTGTTGGAACTAACAATGGTAAAGTTCAGATTTGGGATGCAG 896	GGGGTTCATCGGTTCTGGTAGCAGAGACAAGAGTATTCTTCAGAGAGCATAA GCACACAAGAAGTTTTGTTAAACTGGTCAGACACAAATCAGAGGTTTTGTGGGACTTG GCACACAAGAAGATTTGTTAAATTGGCAGGCTCATAAATCTGAGGTTTTGTGGGACTCAAAAAAAA	920 AGIGGICITAIGACAACAAGAGTAGCATCIGGIGGAAACGACAAIAGGCITIIGIAI 979 1137 GGAATCAACACCAGCCTGTCCTCAAGTACTGTGAGCACACAGTAGCTGTTAAAG 1196 1137 GGAATCAATCAACAACCGGTTTTGAAATATAGTGAACACTGCAGCTGTTAAAG 1039 980 GGAACCATTGACAACCGGTTTTGAAATATAGTGAACTGCAGCTGTTAAAG 1039 1197 CTATTGCATGGTCCTCATCTTTGACATTCTTGCATCTGGAGAACTGCAGATA 1256 1040 CCATTGCTTGGTCTCCTCATGTTCATGGACTTCTTGCTTCTGGTGGTGGTACTGCTGATA 1099	1257 GATGTATTGTTTTTGGAATACCACCACAAACTCACACCTTAGCTGTATGGACACTGGAA 1316

1436

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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Wagnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1459)

Yamada,K., Bath,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,

Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,

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Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,

Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,

Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,

Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Arabidopsis Open Reading Frame (ORP) Clones
1077 AGTGGTCATATGATAACCGTGAGTTGGCATCTGGAGGAAATGACAACAAATTGTTTT 1136
                                                                                            986 AGTGGTCTTATGACAACAGAGCTAGCATCTGGTGGAAACGACAATAGGCTTTTTTGTAT 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY091235 1459 bp mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative Srwl protein (At4g11920) mRNA,
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                                                                                                                                                                                                                                                                            1046 GGAACCAACATTCAACACAGATTTTGAAATATAGTGAACACACAGCAGCTGTTAAAG 1105
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                                                                                                                                                                                                                                                                                          Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualiflers
   The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J. Sarcou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                              Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                         The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUMI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, G.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Meuk, R., Jans, M., Naywen, M., Naywen, M., Yam, C., Lam, B., Lin, J., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
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Pred. No. 2.6e-155;
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Matches 957; Conservative
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; Endsidopsis.

Goldsmith,A.D., iee,J.M., Quach,H.D., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Lam,B., Iin,J., Miranda,M., Narusaka,M., Nguyen,M., Ramiya,A., Sakurai,T., Satou,M., Sekki,M., Shinni,P., Southwick,A., Shinnozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A., Shinnozaki,K., Arabidopsis Pull Length cDNA Clones
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L. Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA , RIKEN Arabidopsis Full-Length CDNA): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Rawai, J., Hayashizaki, Y. and Shinozaki, K.
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                                                                                                          Arabidopsis thaliana putative Srwl protein (At4g11920) mRNA, complete cds.
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Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Cebolla, A., Vinardell, J.M., Olah, B., Kiss, E., Roudier, F., Kodorosi, A. and Kondorosi, E.
The mitotic inhibitor cess2 is required for endoreduplication polyploidy-dependent cell enlargement in plants
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Vinardell, J.M. and Kondorosi, E.
Direct Submission
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VFPSPRGQNTESEIGALSGLGRTIR"
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5572. 5634,5735. 5929,6459. 6560,6651. 6713,6827. .
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Arabidopsis thaliana cell cycle switch protein (At5g13840) mRNA,
CGCCGTCGATGACATTGCCGAATAGGAATATTTTTAGGTATAAGACGGAGACGAGACAGT 2833
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Spermatophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Nguyen, M., Karlin-Neumann, G., Southwick, A., Tripp, M., Miranda, M., Palan, C., Bowser, L., Jones, T., Bahh, J., Carninol, F., Chen, H., Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
Submitted (19-NOV-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J. Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Sh inozaki,K.
                                                                              2954 TTATCTTTTTTTTTTTTTTGATCTTTGATGTTGTTGATTTTAGGGTTTTGATTT
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                                                  654 ----AGGITTTGGATGCACCTGCTTTGCAAGATGATTTTTATCTGAATCTGGTAGATT
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LOCUS

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers

organism="Arabidopsis thaliana"

FEATURES

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CSVQWTREGSYISIGTSHGQVQVWDGTQCKRVRTWGGHQTRTGVLAWNSRILSSGSRD
RNILQHDIRVQSDPVSKLVGHKSEVCGLKMSHDDRELASGGNDNQLLVWNNHSQQPIL
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SKNVNEIVSTHGYSQNQIMLMKYPSMSKVATLTGHSMRVLYLATSPDGGTIVTGAGDE
TLRFWNVFPSVKMQTPVKDTGLWSLGRTQIR"
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                                                                                                                          /note="This clone is in pENTR/SD-dTopo This is a cloned PCR product using RIKEN clone RAFL09-66-B04 (AY099581) as a template
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23.5%; Score 472.4; DB 8;
Best Local Similarity 66.1%; Pred. No. 5.7e-100;
Matches 680; Conservative 0; Mismatches 349;
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                                                                                                     thaliana"
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                                    Location/Qualifiers
   contributed
   (SSP/Stanford)
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana;

SM Arabidopsis thaliana;

SM Arabidopsis thaliana;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1891)

S Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,

Palm,C.J., Bowser,L., Banh,J., Carninci,P., Chen,H.,

Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Carninci,P., Chen,H.,

Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,

Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

Direct Submission

L Submitted (24-APR-2002) DNA Sequencing and Technology Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1319 GCCAGACTATAGTGACCGGAGCAGGAGATGAGACCTGCCGGGTTTTGGAACGTCTTTCCTT
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
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/product="Similar to frizzy-related protein
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.larity 66.2%; Pred. No. 3.3e-84;
Conservative 0; Mismatches 308;
                                                                                                                                                           organism="Xenopus laevis"
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1 (bases 1 to 303)

1 (bases 1 to 303)

Direct Submission

Submitted (23-JAN-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 2082-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis, Similar to frizzy-related protein 1 (Drosophila), clone MGC:53225 IMAGE:5543396, mRNA, complete cds. BC045037
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Context: XGC help desk
Email: cgapbe-remail.nih.gov
Tisaue Procurement: Dr. 1gor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                Sigrist, S.J. and Lehner, C.F.
Drosophila fizzy-related down-regulates mitotic cyclins and is required for cell proliferation arrest and entry into endocycles Cell 90 (4), 671-681 (1997)
                                                                                                                       TTATAGGGTTCTCTATCTTGCCATCTCTCCAGATGGACTAGTTGTAACTGGAGCTGG
                             CAATCTTGTCTGGTCCAAAATGTCAACGAACTAGTAAGCACACATGGGGTACTCCCAGAA
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/organism="Xenopus laevis"
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Xenopus laevis (African clawed frog)
Xenopus laevis
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                                                      Length 2649
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                                                          Score 403.6; DB 5;
Pred. No. 7.9e-84;
0; Mismatches 309;
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823 934

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BC006616 Mus musculus frizzy-related protein 1 (Drosophila), mRNA (cDNA clone MGC:11723 IMAGE:3967009), complete cds.
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Mus musculus
Mus maculus
Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/product="Tubknown (protein for MGC:55450)"

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/db xref="G1:28856200"

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/db xref="G1:28856200"

/craslation="WhODYERPLIRQINVQNDNTSPWKAMOVICHLTPTPESPLSSPS

KHODRETPSRAGANWSTHERA.THERA.THERA.THERASTPDINGSGRADGLAYSALLKNEL

IGAGIEKVLDPOTEDRRILQPSTPERRS.FSYSISARSTPDINGSFPSENSENSO

KILRSPRYPTRISKIPFRYDAPELQDPYLANLYDWSSLNVLSVGGTCVYLWSACT

SQYTRLCDLSVGGSSRDRMILQRDIRTPPLQSERRLQGTROSTGKWSTDHQLLASGG

NUNKLLWWHSSVLPWQYTEHLAVYRATHANSPHQHGILASGGGGTABRCIRFWNTITA

QPLQCIDTGSQVCNLARKSTYRELVSTHGSYSQNQILVWKYPSLTQVAKLTGHSSTRVLY

LAMSPDGRAIVTGAGDETLRFWNVFSKTRSTKESVSVLANLFTRIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USAN WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                    VRT 05-MAR-2003 complete cds.
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
[ (base 1 to 2089)
Strausberg,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 101 Row: h Column: 12. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/mol_type="mRNA"
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/tissue_type="Whole body, adult, (one male ar including unifertilized eggs)"
/lone lib="Sugano Kawakami zebrafish DRA"
/lab_host="Vector: pME18S-FL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 357; DB 5; Length 2089;
Pred. No. 6.7e-73;
0; Mismatches 330; Indels
                                                                                    2089 bp mRNA linear
Danio rerio, clone MGC:55450 IMAGE:2639752, mRNA,
EC048038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 t
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                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
Danio rerio
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Best Local Similarity 63.4%;
Matches 581; Conservative
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                             RESULT 12
BC048038
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AUTHORS
TITLE
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Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marushna, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Ketteman, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Hellen, E., Ketteman, M., Maden, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Voung, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
32188257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
CONtact: MGC help desk
Email: ogapbs-r@mail.nih.gov
Email: ogapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center ocde: BCM-HGSC
Web site: http://www.hgc.bcm.tmc.edu/cdna/
COntact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 17 Row: 1 Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers
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/ Organism="Mus musculus"

/mol type="mgNa"

/strain="FVB/N"

/db xref="taxon:1000"

/clone="MgC:11723 IMAGE:3967009"

/tissue type="mgAmmary tumor. Metallothionien-TGF alpha

model. 10 month old virgin mouse. Taken by biopsy."

/clone="lib="NGI GAPP Mam":

/lab host="mhGI GAPP Mam":

/note="Yector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="synonym: Fyr"
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'db_xref="MGI:1926790"
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gene="Fzr1"
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Strausberg, R.
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AUTHORS
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JOURNAL
                             AUTHORS
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IQCIDTGSQVCRLAWSKHASTKSKTKSTKSSVSVLNLFTRIR"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                1154 CAGCTGTCCTCAAGTACTGTGAGCACACAGCAGCTGTTAAAGCTATGCATGGTCTCCT
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                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                    Score 352.8; DB 10; Length 1861; Pred. No. 6.4e-72; 0; Mismatches 337; Indels 6;
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Best Local Similarity 62.9%;
Matches 581; Conservative 0
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1454 GITCICIAICIIGCCAICICICCAGAIGGACAGACIAITGIAACIGGAGCIGGAGAIGAA 1513
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                                                                                                                                                                                                  TCTGGTGGACGGGATAAGAATATTTATCAACGAGATATACGCCACACAA---GAAGATTTT 1033
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Human homologue of Fizzy-related protein

Published Only in Database (1999)

2. (bases 1 to 1491)

Kotani, S., Oyamatu, T. and Todokoro, K.

Direct Submission

Submitted (19-APR-1998) Kazuo Todokoro, The Institute of Physical
and Chemical Research (RIKEN), Molecular Cell Science Laboratory;
3-1-1, Koyadai, Tsukuba, Ibaraki 305-0074, Japan

(E-mail:todokoro@rtc.riken.go.jp, Tel:81-298-36-9075,
                                                                            878 diadgracacacaadagecrredrecadarendedacetecrededadadadenere 937
818 ICIGIAGAAGGGGACTCAGTGACTICCGTTGGCTGGTCGAGGGGGAACTTGGTCGCA 877
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Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1178 AGCCCTGTGCAGCAGTATACGGAGCACCTGCCAGCAAGGCCATTGCCTGGTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1274 AATACAACCACAAACTCACACCTTAGCTGTATGGACACTGGAAGTCAGGTTTGCAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1298 AACACTCTGACAGGTCAGCCACTGCGGTTGACACAGGCTCACAAGTGTGCAACTG
                                                                                                                    917 TCAATGGAGGGCCATCGGTTACGTGGGGGCCTTGGCCTGGAGTTCATCTCTTTTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                 GTTGGAACTAACAATGGTAAAGTTCAGATTTTGGGATGCAGCAAGATGCAAGAGATAAGA
                                                                                                                                                                                                                                                                                 GTTAGTAAACTGTCAGGACACAAATCAGAGGTTTGTGGACTGAAGTGGTCATATGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCCTGTCCTCAAGTACTGTGAGCACAAGCAGCTGTTAAAGCTATTGCATGGTCTCCT
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AB013462.1 GI:6463678
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MSPDGBALVTGAODSTLAFWNVFSKTRSTKSSTKSSVSVLNLFTRIR"
                                   AF083809 2258 bp mRNA linear ROD 01-SEP-1999
Mus musculus fizzy-related protein (Fyr) mRNA, complete cds.
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            GITCTCTATCTTGCCATCTCTCCAGATGGACAGACTATTGTAACTGGAGCTGGAGATGAA 1513
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                                                                                                                                                                                                                                                                                                                                                Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Musinae, Lo 2258)
Jin, D.-Y. and Jeang, K.-T.
Characterization of mouse fizzy-related protein
Unpublished
2 (bases 1 to 2258)
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Lounitted (12-AUG-1998) LMM, NIAID/NIH, 9000 Rockville Pike,

Bethesda, MD 20892-0460, USA

Bethesda, MD 20892-0460, USA

1. 2258
/ coganiem="Mus musculus"
/ mol type="mRNA"
/ do xref="taxon:10090"

1. 2258
/ Gene="Fyr"

143. :1624
/ gene="Fyr"
/ function="Fyr"
/ function="cell cycle regulator"
/ chan start=1
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Pred. No. 1.5e-71;
0; Mismatches 338; Indels
                                                                                                                    ACCCTGAGGTTCTGGAATGTCTTC 1642
                                                                                             1514 ACGCTTAGGTTCTGGAATGTTTTC 1537
                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                         AF083809.1 GI:5813824
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Best Local Similarity 62.8%;
Matches 580; Conservative
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Pred. No. 4.2e-69;
0; Mismatches 327; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Fizzy-related protein"
                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
!. .1491
                                         Location/Qualifiers
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1. .1491
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	cDNA encoding an a	Human ORFX ORF3013	Drosophila melanog	Candida albicans e	DNA encoding novel	Aspergillus fumiga	Aspergillus fumiga	Aspergillus fumiga
	Ω	AAZ37024	AAC77458	ABL05493	ABZ32308	AAS77749	ABT18274	ABT18868	ABT20688
	80	21	21	23	24	23	20	25	25
	Query Match Length DB ID	2006 2							
æ	Query Match	100.0	16.9	16.7	15.1	13.4	13.2	13.2	13.2
	Score	2006	339.2	334.8	303.8	269.6	263.8	263.8	263.8
	Result No.	; ;! ;	7	m	4	ហ	9	7	80

(CNRS) CNRS CENT NAT RECH SCI.

Aspergillus fumiga	Aspergillus fumiga	Aspergillus fumiga	Drosophila melanog	Drosophila melanog	Drosophila melanog	Drosophila melanog	Drosophila melanog	Arabidopsis thalia	Drosophila melanog	Sequence encoding	breast canc	Lung cancer relate	Lung cancer relate	Oesophagus cancer	Gene CDC20 differe	Human cancer assoc	Sequence encoding	Arabidopsis thalia	Aspergillus oryzae	Drosophila melanog	Drosophila melanog	Corn ear-derived p	DNA encoding novel	Human transcriptio	Toxicologically re	Human ovarian canc	Phase-1 Rat CT gen	Human colon cancer	Human ovarian canc	Candida albicans e	ovarian can	gene expr	ç	Lan	ä	Human ORF2082 cDNA	
ABT20090	ABT17680	49	ABL05492	ABL18423	342	ABL05448	ABL07411	ABZ13183	ABL07410	AAQ96099	ABT11002	ABL65393	ABL65837	ABL67656	ABK35539	AAC77801	AAQ96100	AAC46256	AAF11864	ABL10086	ABL06722	ABX83461	AAS77748	ABN75375	ABZ82891	ABL81366	ABT09540	AAH30586	ABL82189	ABZ32237	ABL81347	ABZ35113	ABX77642	ABL81060	AAT23988	713	
25	25	25	23	53	23	23	23	24	23	16	24	24	24	24	24	21	16	21	21	23	23	25	23	24	25	24	24	21	24	24	24	24	25	24	16	24	j
1993	3398	3993	14283	1369	3369	5058	1706	1344	3852	1767	1686	1686	1686	1686	1686	1688	1700	2697	650	14482	3404	274	574	645	1024	480	672	416	484	1905	457	469	678	480	310	486	; } }
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ALIGNMENTS

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Alfalfa; ccc52Ms; WD40 motif; fizzy-related; fzr subfamily; fzr protein; cellular differentiation; endoreplication; cell proliferation; plant cell; somatic embryogenesis; endoploidy; reserve tissue; in vitro plant regeneration; ss.
                                                                             cDNA encoding an alfalfa fzr protein designated ccc52Ms.
                                                                                                                                                                     Location/Qualifiers
182..1609
/*tag= a
/product= "ccc52Ms"
                   AAZ37024 standard; cDNA; 2006 BP
                                                                                                                                                                                                                                                                  98FR-0007174.
                                                                                                                                                                                                                                                                                      98FR-0007174.
                                                            13-MAR-2000 (first entry)
                                                                                                                                                      Medicago sativa.
                                                                                                                                                                                                                                                                   08-JUN-1998;
                                                                                                                                                                                                                                                                                      08-JUN-1998;
                                                                                                                                                                                                                           FR2779433-A1
                                                                                                                                                                                                                                               10-DEC-1999.
                                       AAZ37024;
                                                                                                                                                                          Key
RESULT 1
          AAZ37024
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Kondorosi A;

Cebolla A,

New plant protein, useful for regulating differentiation and proliferation of plant cells, especially for stimulation of somatic embryogenesis -WPI; 2000-089743/08. P-PSDB; AAY53985. Kondorosi E,

The present sequence encodes an alfalfa protein, designated ccc52Ms.

The protein contains repeated WD40 (Trp-Asp) motifs, and belongs to the far (fizzy-related) subfamily. The WD40 motifs are situated in the far (fizzy-related) subfamily. The WD40 motifs are situated in protein comprises 7 domains, and the last domain, domain 7, contains a potential liaison site for cyclins. The N-terminal region of the protein has a peptide sequence (DRFIPSR) which corresponds to a motif which is conserved in fir proteins. The protein intervenes in the regulation of cellular differentiation, and augments endoreplication. The polymuclocide sequence and its antisense sequences are used to regulate the differentiation and proliferation of plant cells and for stimulating somatic embryogenesis. They are also useful for promoting cendoploidy in plant cells or tissues to increase productivity of central in culture, by increasing the conversion of embryos. Disclosure; Page 21-23; 36pp; French.

Sequence 2006 BP; 555 A; 398 C; 441 G; 612 T; 0 other;

Query Match

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120 120 180 240 240 300 300 360 9 9 Trircascraciariariariasasasirasirasiriariariariariariariariariariaria 241 AccectreAeceatcAeceaeAeAeaecercateAecearateAecea TTACACCTCACCTTCTCGAACAATCTACTCCGATAGGTTCATTCCGAGTAGATCTGCTTC 121 TGCAAAAATTCTTTTACAGCGTTCTTTTTCCCCGGGAAAAAATTAACACAGCTCCGC CATGGACGGAACCGGTAATCGAAATCCACCGACTTCCACCGTCAGAGACAATTCTCC 181 CATGGACGGAACCGGTAATCCAACCACCGACTTCCACCGTCAGAGACAATTCTCC TGCAAAAAATTCTTTTACAGCGTTCTTTTTCCCCCGGGAAAAAATTAACACAGCTCCGC 0; Gaps 100.0%; Score 2006; DB 21; Length 2006; 100.0%; Pred. No. 0; Alsmatches 0; Indels 0; Best Local Similarity 100.0 Matches 2006; Conservative 121 61 181 241 61 301

360 420 420 480 480 540

> GAAATTCGCTTTGTTTGATATCAATACTCCGACAGAAGGACGCGATGATAGTTCCAGCGC GAAATTCGCTTTGTTTGATATCAATACTCCGACAGAAAGGACGCGATGATAGTTCCAGCG

Tracaccrcaccrrcrcaaacaarcracrccaraggrrcarrccaagragarcrgcrrc

301

361 361 421 421

Trataccacterrercacaaaccccricirircaaccccarcircccccricccccria GGAAAAAACCGACTCGCCGTCGATGACATTGCCGAATAGGAATATTTTTAGGTATAAGAC 481 GGAAAAACCGACTCGCCGTCGATGACATTGCCGGAATAGGAATATTTTTAGGTATAAGAC

TIATACGACTETTCTGAGAACGGCGTTGTTTGGACCGGATGTTGCCGGTCCGGTTACGCC

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GGAGACGAGACAGTCCATGCACTCGCTTTTCGCCGTTTATGGATGATGTTTTGTTCCTGG

541

481

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1140 1320 1380 1021 ACAAGAAGATTTTGTTAAACTGTCAGGACACAAATCAGAGGTTTGTGGACTGAAGTG 1080 1081 Grcarargaraaccercargracarcreaagaaaraacaacaarrerrreraa 1140 1141 TCAACACTCAACCCAGCCTGTCCTCAAGTACTGTGAGCACACAGCAGCTGTTAAAGCTAT 1200 1200 1320 1380 1440 1440 1500 1500 1560 1620 1680 TICATCICITITIGICTICIGGIGGACGGGAIAAGAAIAITIAICAACGAGAIAIACGCAC 1020 1021 ACAAGAAGATTTTGTTAGTAAACTGTCAGGACACAAATCAGAGGTTTGTGGGACTGAAGTG 1080 1560 1680 840 999 780 900 901 AIGCAAGAAGAIAAGAICAAIGGAGGCCAICGGIIACGIGICGGGGCCIIGGCCIIGGAG 960 901 Argcaagaagaraagarcaargcagccarcgcraacgroccccraggccraggccraggg 960 661 GGATGCACCTGCTTTGCAAGATTATTTATCTGAATCTGGTAGATTGGTCTTCACACAA 720 841 TGGTACTCATCTTGCTGTTGGAACTAACAATGGTAAAGTTCAGATTTGGGATGCAGCAAG 900 TGTTAATCATAGTCCGGTTAAGGCTCCTAGGAAGGTTCCTCCACGATCGCCTTATAAGGTTTT TGTGTTGGCTGTTGGTTTGGGTAACTGTGTCTTTTGTGGAATGCTTGTAGCAAGGT TGGTACTCATCTTGCTGTTGGAACTAACAATGGTAAAGTTTCAGATTTGGGATGCAGGAAG 1381 CCAGAACCAGATTATTGTTTGGAGATACCCCACTATGTCAAAGCTGGCGACTCTTACCGG 1621 GTTGCAGCCCAATCATGTGGCATATTTCTAAGTTTGGGTTGCTGTGTAGAACTAAATTTC 601 TGTTAATCATAGTCCGGTTAAGGCTCCTAGGAAGGTTCCTCGATCGCCTTATAAGGTTTT 721 TGTGTTGGCTGTTGGGTAACTGTGTCTATCTCTGGAATGCTTGTAGCAGGT 1261 TATTCGTTTTTGGAATACAACCACAAACTCACACCTTAGCTGTATGGACACTGGAAGTCA 1321 GGTTTGCAATCTTGTCTGGTCCAAAATGTCAACGAACTAGTAAGCACACATGGGTACTC CCAGAACCAGATTATTGTTTGGAGATACCCCACTATGTCAAAGCTGGCGACTCTTACCGG 1441 CCATACTTATAGGGTTCTCTATCTTGCCATCTCTCCAGATGGACAGACTATTGTAACTGG 1441 CCATACTTATAGGGTTCTTGCCATCTCTCCAGATGGACGACGACTATTGTAACTGG 1501 AGCTGGAGATGAAACGCTTAGGTTCTGGAATGTTTTCCCTTCCCCTAAATCACAGAATAC 1621 GTTGCAGCCCAATCATGTGGCATATTTCTAAGTTTGGGTTGCTGTGTAGAACTAAATTTC 1261 TATTCGTTTTTGGAATACAACCACAAACTCACACCTTAGCTGTATGGACACTGGAAGTCA 1501 AGCTGGAGATGAAACGCTTAGGTTCTGGAATGTTTTCCCTTTCCCCTAAATCACAGAATAC GGATGCACCTGCTTTGCAAGATGATTTTTTATCTGAATCTGGTAGATTGGT 841 1201 721 781 601 1321 1381 196 1081 1561 ద ò 셤 à g ઠે ద ઠે d à a ò d à d ਨੇ g ò ď ઠે d ö d à g à a ò g ò g à 요 8

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                                                                                                                                                                                                                                                                                                                                                                                    Human, open reading frame, ORFX; detection; cytostatic; hepatotropic;

wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
wationvulsant; otheropolytic; coagulant; vasotropic; antidiabetic;
whypotensive; dermatological; immunosuppressive; antidiabetic;
whypotensive; dermatological; immunosuppressive; antidiabetic;
wationization therapy; cancer; proliferative disorder; hypertension;
munianaemic; gene therapy; cancer; proliferative disorder; hypertension;
munianaemic; gene therapy; cancer; proliferative disorder; hypertension;
wardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
wallergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
bone danage; contraceptive; ss.
                                                                                     ATTCCTGCATTCATGTGTAGTCTCATTTTATATTGAAAAGATGATAACAAATGGGTAATT 1860
                                                                                                      reagcegagaacaccaregregaaaaaccrreaarararaaaacaccaccaaagragcarc 1740
                                           TITIACCAACTGGGAGGCCTTGGAGGGAGCTATAAAAGTTTTGATATGGCTGCCGGTGAT
                                                              triaccaacteggagagccrrgagagagagararaaagrrrrgararggcrgccggrgar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                  Human ORFX ORF3013 polynucleotide sequence SEQ ID NO:6025.
                                                                                                                                                                                                                        TAACAGAGAAAAAAAAAAAAAA 2006
                                                                                                                                                                                                                                            1981 TAACAGAGAAAAAAAAAAAAAA 2006
                                                                                                                                                                                                                                                                                                     AAC77458 standard; cDNA; 5905
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA, Leach M;
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
continuotsimilant; cardiant; thrombolytic; coaquilant; vasotropic;
immunostimilant; cardiant; thrombolytic; coaquilant; vasotropic;
antidabetic, hypotensive; dermatological; immunosuppressive;
contidabetic, hypotensive; dermatological; immunosuppressive;
antidabetic, hypotensive; dermatological; immunosuppressive;
contidabetic, hypothyroidism encological; immunodeficiency (SCID), AIDS, viral,
bacternal on hypothyroidism, cholesterol ester actorage, systemic;
continual haemoglobinuria, antidifiammatory disease; to enhance
nocturnal haemoglobinuria, antidifiammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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5; Page 5206-5209; 5507pp; English.
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                 Claim
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1384 GGCGGCACAGCTGACCGCTGTATCCGCTTCTGGAACACGCTGACAGGACAACCACTGCAG 1443
                                     TGTATGGACACTGGAAGTCAGGTTTGCAATCTTGTCTGGTCCAAAAATGTCAACGAACTA 1360
                                                                        1444 rerarceacacececcaacreceaareresecresecereseceaaceceaaceaceceaaceae
                                                                                                                GTAAGCACACACGCTACTCCCAGAACCAGATTATTGTTGGAGATACCCCACTATGTCA 1420
                                                                                                                                           1421 AAGCTGGCGACTCTTACCGGCCATACTTATAGGGTTCTCTATTGCCATCTCTCCAGAT 1480
                                                                                                                                                                                                                        1564 CAGGIGGCCAAGCIGACGGGGACTCCIACGGGIGCIGIACIGGGAAIGICCCCTGAI 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeuticis and pharmaceutical furge. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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16.7%; Score 334.8; DB 23; Length 2645; Second Best Local Similarity 61.5%; Pred. No. 1.5e-67;
Matches 572; Conservative 0; Mismatches 352; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                    GGACAGACTATTGTAACTGGAGCTGGAGATGAAACGCTTAGGTTCTGGAATGTTTT 1536
                                                                                                                                                                                                                                                                                             1624 GGGGAGGCCATCGTCACTGGTGCTGGAGACGAGACCCTGAGGTTCTGGAACGTCTT 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 10961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila, developmental biology, cell signalling, insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 10961; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-0614150.
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P-PSDB; ABB61390.
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                          1002 TTGCAGGACGACTTCTATCTGAACCTGGTCGACTGGTCGTCGTGGACGTACTGGCTGTA 1061
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CCGGTTAAGGCTCCTAGGAAGGTTCCTCGATCGCCTTATAAGGTTTTGGATGCACCTGCT 673
                                                                            674 TIGCAAGAIGAITITIAICIGAAICIGGIAGAITGGICTICACAAAGAIGGCIGTI
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ABZ32308 standard; DNA; 1794 30-JAN-2003 (first entry) ABZ32308; ABZ32308 ID ABZ3 XX AC ABZ3 XX DT 30-J RESULT 4

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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion; of a promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes to the aurivial or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulares the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional compound catabolism, biosynthetic, transporter, transcriptional compound is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for translational, signal transduction, DNA replication and cell aivision activity. The method is useful for identifying a compound having the custorist in infection by C. albicans. The present sequence is that of an essential candida albicans gene used in the method of the invention. Note: The sequence data for this pased on sequence information supplied to Derwent by the process.
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signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constructing strains for identifying gene products as effective for therapeutic intervention, by inactivating in the strain one of a gene and placing other allele of the gene under conditional expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 37; SEQ ID NO 6595; 167pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL;
                  Candida albicans essential gene SEQ ID NO 6595
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20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
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Matches 536; Conservative
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P-PSDB; ABP73758.
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Best Local 9
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GGTTTGGGTAACTGTGTTTTTCTCTGGAATGCTTGTAGCAGGCAAGGTAACTAAATTATGT
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27-APR-2001; 2001US-287066P.
05-UTN-2001; 2001US-295890P.
09-UTL-2001; 2001US-316362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fungicide; cytostatic; cancer; contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B, Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus fumigatus
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llarity 62.6%; Pred. No. 2.1e-52;
Conservative 0; Mismatches 259; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 13553; 103pp; English
                                                                                                                                                                                        Tang YT;
                                                    30-MAR-2001; 2001WO-US08631.
                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                        Liu C,
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essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds. The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polymucleotides are useful for δ New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer SM; Lemieux Hu W,

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expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. timigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify protential orthologous essential or virulence genes for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an artispen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polyuncheotides encoding the other protein with which binding occurs or to identify inhibitors of the binding cours or to identify inhibitors of the binding clicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host issues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence to reside actions. This polynucleotide sequence represents one of the essential constants.
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Aspergillus fumigatus, useful for treating or preventing infections ?
A. fumigatus, or for treating a non-infectious disease in a subject
e.g. cancer -
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27-APR-2001; 2001US-287066F.
05-JUN-2001; 2001US-295890P.
09-JUL-2001; 2001US-303899F.
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sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raleing anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantizatively determine levels of the protein in biological fluids, as a marker for host rissues in which pathogenic organism invade or reside, and to host tissues in which pathogenic organism invade or reside, and to factoria. This polymucleotide sequence represents one of the essential genes of Appergillus fumigatus of the invention.
biochemical activity and/or function, for comparing with
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Sequence 1398 BP; 368 A; 360 C; 343 G; 327 T; 0 other;

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1060 TITIGICITCTGGTGGACGGGATAAGAATATTTATCAACGAGATATACGCACACAAGAAG 1028 1088 1000 1268 rcreshacacrecracrestricacrearcaassaasirearacesesiasecaesisista 1120 940 Archircanadeacheceaaacherrehacadaharecandeadacandeece 700 968 820 880 400 668 460 TTTGCGAACTAAGAGATGATACTGTCACAAGTGTTAGCTGGATTCAGAGGGTAATGAGAT 580 848 ATCTTGCTGTTGGAACTAACAATGGTAAAGTTCAGATTTGGGATGCAGCAAGATGCAAGA 908 grerreeccrasseaarreasreracarsresaarresaarakeessaessiskeakake 520 recrracercaeerrereedareeacrearerrecaecercarerreerreerre 1029 ATTITIGITAGIAAACIGICAGGACACAAAICAGAGGITIGIGGACIGAAGIGGICAIAIG Argagacaccerrrarcecrrcicgaccaracecaeccergaagecerracr TTTGGAATACAACCACAAACTCACACCCTTAGCTGTATGGACACTGGAAGTCAGGTTTGCA -----TGTTTGTTCTGTTGGGCTCAACGTGGTACTC 909 AGATAAGATCAATGGAGGGCCATCGGTTACGTGGGGGGCCTTGGGCCTGGAGTTCATCTC CAACCCAGCCTGTCCTCAAGTACTGTGAGCACACAGCAGCTGTTAAAAGCTATTGCATGGT CTGCTTTGCAAGATGATTTTTATCTGAATCTGGTAGATTGGTCTTCACACAATGTTGG CTGTTGGTTTTGGGTAACTGTGTCTTTGTATGCTTGTAGCAAGGTAACTAAAT 581 Trcrcrararerrescaarearrarrarererrerreareacrescarrissacacaeseseaca ATAGTCCGGTTAAAGGCTCCTAGGAAGGTTCCTCGATCGCCTTATAAGGTTTTGGATGCAC 341 AGACTCCTCGCAAGCAGCCTCGCTAAATAAAGTACCCTATAAGGTTCTCGACGAC cceaririscaagargarricracrisaarcresresacresecagragraardrecras Gaps 60; DB 25; Length 1398; Query Match
13.2%; Score 263.8; DB 25; Length
Best Local Similarity 56.3%; Pred. No. 3.4e-51;
Matches 557; Conservative 0; Mismatches 372; Indels TATGTGATTTGGGGGTTGATGATTG------1149 941 1001 1269 1001 701 969 191 609 401 729 461 789 521 849 641 699 814

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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a confection comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of other related or distant pathogenic organisms trelated or distant pathogenic organisms trelated or distant pathogenic organisms to identify applicated genes or paralogues having the same or similar blochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify pathomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antipodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding
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27-APR-2001; 2001US-287066F.
05-UUN-2001; 2001US-295890P.
09-UUL-2001; 2001US-303899P.
31-AUG-2001; 2001US-316362P.
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interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to stolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention.
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Best Local Similarity 56.3%;
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat a non-infectious by a pathogenic corganism such as A. fumigatus, to prevent or contain contamination of an object whisis thingatus, or to prevent or contain contamination of an object comprising A. fumigatus. The polymucleotides are useful for expressing recombinant protein for characterisation, screening or characterisation, screening or characterisation, screening or corganisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify or distant pathogenic organisms to identify operatial or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an origen to raise anti-DNA antibodies or to elicit another immune response, and for identify inhibitors of the binding occurs or to identify inhibitors of the binding occurs or to identify inhibitors of the binding occurs or to identify inhibitors of the binding occurs or to elicit immune response, as a reagent in assays designed to quantitatively corder manice levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to
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Aspergillus fumigatus, useful for treating or preventing infections
A. fumigatus, or for treating a non-infectious disease in a subject
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cancer; contamination;
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llarity 56.3%; Pred. No. 4.5e-51;
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or
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isolate correlative receptors or ligands in the case factors. This polynucleotide sequence represents one genes of Aspergillus fumigatus of the invention.
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fundatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic corganism such as A. fundatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or inhibit formation of an object of a concer), to prevent or inhibit formation of an object of a concer), to prevent or inhibit formation of an object of a concer), to prevent or inhibit formation of an object of a concerning or therapeutic use, as markers for host tissues in which the pathogenic expressing recombinant protein for characterisation, screening or corganisms invade or reside, for comparing with the DNA sequence of A. fundatus to identify duplicated genes or paralogues having the same or corganisms to identify duplicated genes or paralogues having the same or constant biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify and or distant pathogenic organisms to identify operation or distant pathogenic organisms to identify of concerning and or distant pathogenic organisms to identify of potential or virulence genes for selecting and one axis and for identifying polynucleorides encoding the other protein corresponse, and for identifying polynucleorides encoding the other protein with which binding occurs or to identify inhibitors of the binding occurs or to identify inhibitors of the binding occurs or to identify inhibitors of the binding occurs or to identify inhibitors of the binding occurs or to identify inhibitors of the binding occurs or identify inhibitors of the binding occurs or identify inhibitors of the binding occurs or identify inhibitors or the binding occurs or identify inhibitors or the polypeptides may be used to raise antibodies and to host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence of factors. This polymucleoride s

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essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds.
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Aspergillus fumigatus, useful for treating or preventing infections
A. fumigatus, or for treating a non-infectious disease in a subject
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                               fumigatus essential gene #1852.
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27-APR-2001; 2001US-287066P.
05-UUN-2001; 2001US-295890P.
09-UUL-2001; 2001US-316389P.
31-AUG-2001; 2001US-316362P.
                                                                                                                                                                                      ABT19494 standard; DNA; 3993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins
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12.9%; Score 259; DB 23; Length 1
Best Local Similarity 60.4%; Pred. No. 9.3e-50;
Matches 446; Conservative 0; Mismatches 290; Indels
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and o
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention issetul in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL04840-ABL16175) and the encoded proteins (ABBS7737-ABB72072).

The sequence acts for this patent did not form part of the printed specification, but was obtained in electronic format directly from wipo at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 1.5e-47;
0; Mismatches 400;
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Sequence 74, Appl Sequence 114, Appl Sequence 4, Appli Sequence 1, Appli Sequence 10, Appli Sequence 5, Appli Sequence 10, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli	Cycle Protein	Score 200.4; DB 3; Length 1767; Fred. No. 9.7e-42; Mismatches 421; Indels 15; Gaps 2; TCGAPICGCATARAGGTTTGGATGCACTGCTTTGCAA 679
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GENERAL INFORMATION:
APPLICANT: Weinstein, Jasminder
TITLE OF INVENTION: Novel Mammalian Cell Cycle Protein
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc./Patent Operations/RBW
STREET: 1840 Dehavilland Drive
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLOPSY MISK
HEDIUM TYPE: PLOPSY MISK
SOFTWARE: PATENTIN Release #1.0, Version #1.25
FILING DATE:
CLASSIFICATION NUMBER: PCT/US95/01806
FILING DATE:
CLASSIFICATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
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Length 1767;

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GENERAL INFORMATION:
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                    TITLE OF INVENTION: No. 6291642el Mammalian Cell Cycle Protein FILE REFERENCE: 0643.0056-04; A-283 D CURRENT APPLICATION NUMBER: US/08/989,856B CURRENT FILING DATE: 1997-12-11 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3 LENGTH: 1700
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     APPLICANT: Weinstein, Jasminder
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ACTTATAGGGTTCTCTATCTTGCCATCTCTCCAGATGGACAGACTATTGTAACTGGAGGT
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                                                                                                                                                                                                                                                       Sequence 3, Application PC/TUS9501806
GENERAL INFORMATION:
APPLICANT: Weinstein, Jasminder
TITLE OF INVENTION: Novel Mammalian Cell Cycle Protein
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISM PC comparatible
COMPUTER: LEW PC comparatible
COMPUTER: DEACHIN RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01806
FILING DATE:
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%; Score 198.8; DB 5; 52.7%; Pred. No. 2.4e-41; ative 0; Mismatches 422;
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSER: Amgen Inc./Patent Operations/RBW STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California COUNTRY: USA
                                                                                             1505 GGAGATGAAACGCTTAGGTTCTGG 1528
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SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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Best Local Similarity 52.7
Matches 487; Conservative
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PCT-US95-01806-3
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PCT-US95-01806-3
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Sequence 6283, Application US/09313294A

Sequence 6283, Application US/09313294A

Sequence 6283, Application US/09313294A

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600
                 GCTGTATGGACACTGGAAGTCAGGTTTGCAATCTTGTCTGGTCCAAAAATGTCAACGAAC 1358
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Sequence 1, Application US/08204675

Patent No. 5677700

GENERAL INFORMATION:

APPLICANT: Boeke, Jef D.

APPLICANT: Boeke, Jef D.

APPLICANT: Boeke, Jef D.

APPLICANT: Boeke, Jef D.

TITLE OF INVENTION: In Vitro Transposition of Artificial TITLE OF INVENTION: Transposons

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSER: Banner, Birch, McKie, and Beckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY; misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351538H1
US-09-313-2944-6283
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COMPUTER READABLE FORM:
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
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ORGANISM: Zea mays
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SEQ ID NO 6283
LENGTH: 288
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Sequence 1921, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILLE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILLING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 1921
LENGTH: 274
                                                                     1037 AGTAAACTGTCAGGACACAAATCAGAGGTTTGTGGACTGAAGTGGTCATATGATAACCGT 1096
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) OTHER INFORMATION: Incyte ID No. 6476212 700551746H1

) NAME/KEY: unsure

! LOCATION: 22, 41, 47, 49, 53

) OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-1921
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CURRENT APPLICATION DATA:
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PETGNI No. S843772

GENERAL INFORMATION:
APPLICANT: Braiterman, Lelita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: In Vitro Transposition of Artificial
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE 
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,675
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTONEY/AGENT INPORMATION:
NAMB: REGISTRATION NUMBER: 32,141
REFERENCE/POCKET NUMBER: 32,141
REFERENCE/POCKET NUMBER: 32,141
REJEPAK: 202.508.910
TELEPHONE: 202.508.910
TELEPHONE: 202.508.929
TELEX: 202.508.929
TELET: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-1
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US-08-766-364-1
; Sequence 1, Application US/08796364
; Patcher No. 5968785
; GENERAL INFORMATION:
; APPLICANT: Devine, Scott E.
; APPLICANT: Borde, Jef D.
; APPLICANT: Braiterman, Lelita T.
; TITLE OF INVENTION: In Vitro Transposition of Artificial
; TITLE OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE Banner, Birch, McKie, and Beckett
; STREET: 101 G Street, N.W.
; CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,754
FILING DATE:
CLASSIPICATION DATA:
CLASSIPICATION NUMBER: US/08/660,754
FILING DATE:
FILING DATE:
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COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002 AAAA 2005
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IMMEDIATE SOURCE:
CLONE: PAT-1
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFRENCE/DOCKET UNMERR: 0110'
TELECOMMUNICATION INFORMATION:
NAME: Kagan, Sarah A.
REGIENATION NUMBER: 32,141
REPERRICE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELERAN: 202.508.910
TELERX: 197430 BBMB UT
INPORMATION FOR ERQ ID NO: 1:
SEQUENCE CHARACTERICTICS:
LENGTH: 4164 base pairs
                                                                                                                                                                             Query Match
2.3%;
Best Local Similarity 53.3%;
Matches 98; Conservative C
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; CLONE: PAT-1
PCT-US95-02520-1
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US-08-204-675-2
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GENERAL INFORMATION:

APPLICANT: The Johns Hopkins University

TITLE OF INVENTION: In Vitro Transposition of Artificial

TITLE OF INVENTION: Transposons

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie, and Beckett

CITY: Washington

STARE: D.C.

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46.4; DB 2; Length 4164;
Pred. No. 0.035;
0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATIG SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US95/02520
FILING DATE: 02-MAR-1995
CLASSIFICATION:
                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RAGAN, SATAN A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.45501
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9100
TELER: 197430 BSWB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
                                                                                                                                                                             01107.45501
           APPLICATION NUMBER: US/08/796,364
                                                                                                                                                                                                                                                                                                                                                              . TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%;
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Best Local Similarity 53.3
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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3901 Grāaagracēcritrigrīgāaatititirāaaccrirgititatīritititītītīcaircc 3960
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                                                                      Gaps
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Sequence 2, Application US/08204675

Batent No. 5677170

GENERAL INFORMATION:
APPLICANT: Boeke, Jef D.
APPLICANT: Boeke, Jef D.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: IT Annaposons
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: 8
ADDRESSEE: Bannar, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
Score 46.4; DB 5; Length 4.1
Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,675
FILING DATE: 02-MAR-1994
                                                                      0; Mismatches
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-660-754-2

Sequence 2, Application US/08660754

Patent No. 5843772

Patent No. 5843772

APPLICANT: Devine, Scott E.

APPLICANT: Braiterman, Lelita T.

ITILE OF INVENTION: In Vitro Transposition of Artificial

TITLE OF INVENTION: Transposons

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie, and Beckett

STREET: 1001 G street, N.W.

STARET: D.C.
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                              2.3%; Score 46.4; DB 1; Length 4933; 53.3%; Pred. No. 0.037; tive 0; Mismatches 86; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: DEACHCIN Release #1.0, Version #1.25
SOSTANEN: DEACHCIN Release #1.0, Version #1.25
SOSTANEN: APPLICATION DATA:
APPLICATION NUMBER: US/08/660,754
FILING DATE:
CLASSITICATION DATA:
APPLICATION NUMBER: US 08/60,754
FILING DATE:
TASSICATION NUMBER: US 08/60,754
FILING DATE:
APPLICATION NUMBER: US 08/60,754
FILING DATE: OZ-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.45501
TELECOMMINICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEPHONE: 202.508.9100
TELERA: 202.508.929
TELEX: 197430 BENB UT
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE. "
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.33
Matches 98; Conservative
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; IMMEDIATE SOURCE:
; CLONE: PAT-2
US-08-204-675-2
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US-08-660-754-2
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APPLICANT: Boeke, Jef D.
APPLICANT: Braiterman, Lelita T.
APPLICANT: Braiterman, Lelita T.
APPLICANT: OF INVENTION: IN Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: ADDRESSEE: N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAMB: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/COCKET NUMBER: 01107.45501
TELEPHONE: 202.508.910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
ZONOT ZIP. 20001
ZONOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-796-364-2
; Sequence 2. Application US/08796364
; Patent No. 5968785
; GENERAL INFORMATION:
TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: dircular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE
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                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002 AAAA 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4790 TAAA 4793
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                                                                                                                                                                                                                                        Score 46.4; DB 5; Length 4933; Pred. No. 0.037; 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09890848
; Sequence 16, Application US/09890848
; Patent No. 6573053
; GENERAL INFORMATION:
APPLICANT: Filth, Greg
APPLICANT: Filth, Greg
CURRENT GOGGTA, Rajesh Muru
TITLE OF INVENTION: Analysis Method
FILE REFRENCE: PA99033
; CURRENT FILING DATE: 2001-08-03
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: ECT/GB00/00346
; PRIOR APPLICATION NUMBER: EP 99300873.9
; PRIOR APPLICATION NUMBER: EP 99300873.9
; NUMBER OF EEQ ID NOS: 18
; SEQ ID NO 16
; LENGTHARE: PatentIn Ver. 2.1
; SEQ ID NO 16
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ORGANISM: Artificial Sequence
                                          DNA (genomic)
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.3%;
Matches 98; Conservative
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                                    MOLECULE TYPE: DNR
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-2
PCT-US95-02520-2
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US-09-890-848-16
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Sequence 2, Application PC/TUS9502520
Sequence 2, Application PC/TUS9502520
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER RADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION:
CLASSIFICATION:
CLASSIFICATIO
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NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.49245
TELECOMMUNICATION INFORMATION:
TELEFAX: 202.508.9100
TELEFX: 202.508.9299
TELEX: 197430 BBMB UT
INFORMATION FOR EQ. DI NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: INCLES: double
STRANDEDNES: double
TOPOLOGY: circular
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4933 base pairs TYPE: mucleic acid STRANDEDNESS: double TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO INMEDIATE SOURCE: CIONE: CIONE:
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Best Local Similarity 53.3%;
Matches 98; Conservative
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US-08-796-364-2
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January 23, 2004, 19:53:14; Search time 713 Seconds (without alignments) 10062.272 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2356869 seqs, 1788235258 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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2006
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 27884, A	Sequence 6595, Ap	Sequence 26005, A	Sequence 26011, A	Sequence 26013, A	Sequence 36526, A	Sequence 1038, Ap	Sequence 2038, Ap	Sequence 7038, Ap			Sequence 5038, Ap	45642	Sequence 988, App	Segmence 988, App
ΩI	US-10-369-493-27884	US-10-032-585-6595	US-10-369-493-26005	US-10-369-493-26011	US-10-369-493-26013	US-10-369-493-36526	US-10-128-714-1038	US-10-128-714-2038	US-10-128-714-7038	US-10-128-714-6038	US-10-128-714-38	US-10-128-714-5038	US-10-369-493-45642	US-09-938-842A-988	TIS-09-938-842A-988
DB	12	13	12	12	12	12	15	15	15	15	15	15	12	10	12
Length	1143	1794	1312	1312	1312	1116	1398	1398	1875	1993	3398	3993	1701	1344	1344
% Query Match	16.3	15.1	13.8	13.8	13.8	13.2	13.2	13.2	13.2	13.2	13.2	13.2	11.2	10.6	10.6
Score	326.2	303.8	277	277	277	264.6	263.8	263.8	263.8	263.8	263.8	263.8	225.6	213.6	213.6
Result No.		8	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	2.

Sequence 25788, A sequence 25, Appli Sequence 107, Appli Sequence 107, Appli Sequence 107, Appli Sequence 1147, Appli Sequence 124, Appli Sequence 27477, A sequence 643, Appli Sequence 643, Appli Sequence 598, Appli Sequence 12508, A Sequence 2567, Appli Sequence 2567, Appli Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 22512, Appli Sequence 22512, Appli Sequence 22512, Appli Sequence 22512, Appli Sequence 22512, Appli Sequence 22512, Appli Sequence 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512, Application 22512,	1808, 1808, 7059, 7059,
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93-27884 27884, Application US/10369493 on No. US20030233675A1 MYORWATION: TI Cao, Yongwei TI Slater, Steven C. TI Goldman, Barry S. TI Chen, Xianfeng TI Chen, Xianfeng TI Chen, Xianfeng TI Chen, Stanfeng TI Ch	Score 326.2; DB 1 Pred. No. 5.9e-72; 0; Mismatches 343	ACCT	-61 -03 -03	GGCT	-9 -9	ATTA
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1-493-27884 1: 27884, Application US/10 1: LINDORMATION: ANT: Cao, Yongwei ANT: Cao, Yongwei ANT: Slater, Steven C. ANT: Chen, Manfeng CO INVENTION: BLARY S. ANT: Chen, Manfeng CO INVENTION: BLARY WITH ERFERENCE: 38-10 (2205.) TO FIVENTION: PLANTS WITH ERFERENCE: 38-10 (2205.) THE FILING DATE: 2003-02-28 APPLICATION NUMBER: US 60/ RING DATE: 2003-02-21 THING DATE: 2003-02-21 NO 27884 NO 27884 HH: 1143 115M: Neurospora crassa 115M: Neurospora crassa	16.3%; 61.2%; ive	TTGG	-13 -14 -14	AATG	AACG	GTAA
7884 Application o. US2003236/ MATION: ao. Yongwei Hinkle, Gregory Slater, Steven Goldman, Barry Chen, Xianfeng ENTION: EXPRESE ENTION: EXPRESE ENTION: WAD FLANT CE: 38-10 (52057) I.CATION NUMBER: US DATE O. DATE: 2002-02-02-02-03-03-03-03-03-03-03-03-03-03-03-03-03-	16. larity 61. Conservative	GGTT	96TG	ACAC	- 2355	CAAG
44, Appli 6. US200 MATION: HIN, END HIN, END HIN, END Slater, Slater, Slater, Slater, Chen, Xi Chen, Xi	arit	ATAA	TTAA	CTTC	GGAG	GCAG
3-27884 7844, Appli n No. US200 IRORMATION: Cao, Yong:	imil.	CCTT	_5 _5	TGGT	-15 -15 -15	TGTA
193-27 27884 277884 11: Cav 11: Cav	cch al Siπ 545;	647	247	707	307	. 191
RESULT 1 US-10-369-493-27884 Sequence 27884, Application US/10369493 Sequence 27884, Application US/10369493 GENERAL INFORMATION: APPLICANT: Cao, Yongwei APPLICANT: Slater, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICRO TITLE OF INVENTION: PLANTS WITH IMPROV FILE REPERENCE: 38-10 (5205)8 TITLE OF INVENTION: PLANTS WITH IMPROV FILE REPERENCE: 38-10 (5205)8 CURRENT APPLICATION WUMBER: US 60/360,039 PRIOR PILING DATE: 2003-02-28 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 27884 TYPE: DAA TYPE: DAA CREANISM: Neurospora crassa US-10-369-493-27884	Query Match Best Local Similarity Matches 545; Conser	-		•	• •	
RESULT 1 US-10-369 SEQUENCE SEQUENCE SEQUENCE APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLI	Query Ma Best Loc Matches					
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Sequence 6595, Application US/20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Gharles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 10182-005-999
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 5595
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US-10-369-493-26005
Sequence 26005, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

Score 303.8; DB 13; Length 1794;

Query Match

1211

1271

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52022)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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1092 AAATTGTTACTACTCATGGTTTTGCAAAAACCAAGTATCCTTATGGAAATATCCTTCAT 1151
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                                                                                                                                                   CAGATGGACAGACTATTGTAACTGGAGCTGGAGATGAAACGCTTAGGTTCTGGAATGTTT
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Pred. No. 1.9e-59;
); Mismatches 390;
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ORGANISM: Schizosaccharomyces pombe
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SEQ ID NO 26011
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Best Local Simi
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                                              APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPRESENCE: 38-10 (52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 26005
LENGTH: 1312
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Pred. No. 1.9e-59;
0; Mismatches 390;
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CRGANISM: Schizosaccharomyces pombe
US-10-369-493-26005
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Best Local Similarity 56.7%;
Matches 511; Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Gidthe, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 10/1369, 493
CURRENT APPLICATION NUMBER: US 60/360, 039
PRICA PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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Sequence 36526, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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Sequence 26013, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Geo., Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, WITH IMPROVED PROFERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROFERTIES

TITLE OF INVENTION: BARRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

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APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Escabkin, Alexey M
APPLICANT: Lemieux, Sebsatien M
APPLICANT: Lemieux, Sebsatien M
APPLICANT: Lemieux, Sebsatien M
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APPLICANT: Lemieux, Sebsatien M
APPLICANT: Louis-1018-999
CURRENT PILING DATE: 2002-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR PILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
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Pred. No. 4.3e-56;
); Mismatches 372; Indels 60;
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RESULT 7
US-10-128-714-1038
'Sequence 1038, Application US/10128714
', Publication No. US20030119013A1
', GENERAL INFORMATION:
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-1038
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Best Local Similarity 56.3%;
Matches 557; Conservative (
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1038
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US-10-128-714-7038
; Sequence 7038, Application US/10128714
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APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Tishkeff, Daniel
APPLICANT: Tishkeff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemient, Sebastien M
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APPLICANT: Lemient, Sebastien M
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
FILIS REFERENCE: 2002-04-23
FRIOR APPLICATION NUMBER: US 60/285,697
FRIOR FILING DATE: 2001-04-27
FRIOR FILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-06-05
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FRIOR FILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-06-05
FRIOR FILING DATE: 2001-08-31
NUMBER: PREQUIN NUMBER: US 60/316,362
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOOTWARE: PARENTH VEFFIN VUMBER: US 60/316,362
FRIOR FILING DATE: 2001-08-31
SEQ ID NO 2038
FRIOR FILING DATE: 2001-08-31
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FRIOR FILING DATE: 2001-08-31
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Query Match
13.2%; Score 263.8; DB 15; Length 1398; Secore 263.8; Pred. No. 4.3e-56;
Matches 557; Conservative 0; Mismatches 372; Indels 60; Gaps
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US-10-128-714-2038
Sequence 2038, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
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APPLICANT: Tishkoff, Daniel
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APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Alexey M
APPLICANT: Zamudio, Alexey M
APPLICANT: Zamudio, Careary M
APPLICANT: Lemieux, Sebastien M
ITILE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 1018-018-999
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR PILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-04-09
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Pred. No. 5.3e-56;
0; Mismatches 372;
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Publication No. US20030119013A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 557; Conserv
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Pred. No. 5.1e-56;
0; Mismatches 372;
                                                               APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tandio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essent
TITLE OF INVENTION: Methods of Use
TITLE REFERENCE: 1018-0918-99
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PLING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2001-04-29
PRIOR PLICATION NUMBER: US 60/285,697
PRIOR PLICATION NUMBER: US 60/285,697
PRIOR PLING DATE: 2001-04-29
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Best Local Similarity 56.3%;
Matches 557; Conservative
           No. US20030119013A1
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LENGTH: 1875
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US-10-128-714-38
Sequence 38, Application US/10128714
Sequence 18, Application US/10128714
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
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APPLICANT: Broshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: MORBER: US/10/128,714
CURRENT APPLICATION NUMBER: US/202-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR PILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/316,362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 263.8; DB 15; Length
Pred. No. 7.2e-56;
0; Mismatches 372; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.3%;
Matches 557; Conservative
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Publication No. US20030233675A1

Publication No. US20030233675A1

SEREMEAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Greeory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
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                                                                                                                                                                                                             ATCTTGCTGTTGGAACTAACAATGGTAAAGTTCAGATTTGGGATGCAGCAAGAAGA
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APPLICANT: Jiang, Bo

APPLICANT: Tishoff, Daniel

APPLICANT: Tishoff, Daniel

APPLICANT: Tishoff, Daniel

APPLICANT: Zamudio, Carlos

APPLICANT: Zamudio, Carlos

APPLICANT: Lemient, Sebastien M

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APPLICANT: NUMBER: 0182-018-999

FILE OF INVENTION: Methods of Use

FILE OF INVENTION: Methods of Use

FILE OF INVENTION: Methods of Use

FILE PERFENCE: 2001-04-23

FRICR APPLICATION NUMBER: US 60/285,697

FRICR PILING DATE: 2001-04-27

FRICR PILING DATE: 2001-04-27

FRICR PILING DATE: 2001-06-05

FRICR PILING DATE: 2001-06-05

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FRICR PILING DATE: 2001-06-05

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FRICR FILING DATE: 2001-06-05

FRICR FILING DATE: 2001-08-31

NUMBER: VS SEQ ID NOS: 8603

SOGTWARE: PATENTIN VERSION 3.1

SEQ ID NO 5038

LEMIGH: 3993

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Pred. No. 7.9e-56;
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9-10-128-714-5038
; Sequence 5038, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INPORMATION:
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Pred, No. 2.3e-46;
); Mismatches 434;
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 1701
                                                                                                                                                                     TYPE: DNA ORGANISM: Saccharomyces cerevisiae
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APPLICANT: ALBY, VOOT
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APPLICANT: ALBY, VOOT
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 888
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pred. No. 2.2e-43;
0; Mismatches 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 988, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
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US-09-938-842A-988
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Best Local Similarity 54.2%;
Matches 513; Conservative
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Search completed: January 23, 2004, 23:19:37
Job time : 721 secs
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
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APPLICANT: Kreps, Joel
APPLICANT: Wing, Xun
APPLICANT: TIL, Ton
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USB
FILE REFRENCE: SCRIP1300-3
FILE OF INVENTION: OF SAME, AND METHODS OF USB
FILE REFRENCE: 2001-09-24
FRIOR PRILING DATE: 2001-09-24
FRIOR PRILING DATE: 2001-09-24
FRIOR PRILING DATE: 2001-01-16
FRIOR PRILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-01-16
FRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NOS: 5379
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Medicago truncatula/Glomus versiforme mixed BST library Medicago truncatula/Glomus versiforme mixed BST library Eukaryota; mixed BST library Eukaryota; mixed BST libraries. 1 (bases I to 759)
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And Francison, M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTS from roots of Medicago truncatula after colonization with Unpublished Contact: Harrison M.J.
EST481891 MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone pWHAM-14817 5' end, mRNA sequence.
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The Samuel Roberts Noble Foundation
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The Samuel Roberts Noble Foundation
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Pabales; Pabaceae; Papilionoideae; Trifolieae;
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1 (bases 1 to 630)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula flower library
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Medicago truncatula cDNA clone
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  GGAGAGCCTTGGAGGGAGCTATAAAAGTTTTGATATGGCTGCCGGTGA----TATTCCTG
                                                                                         AAACGCITAGGITCIGGAATGITTCCCTICCCCTAAAICACAGAATACTGAAAGIGAAA
                                                                                                           GGGTTCTCTATTGCCATCTCTCCAGATGGACAGACTATTGTAACTGGAGCTGGAGATG
                                                            GGGTTCTCTATCTTGCCATCTCTCCGGATGGACAGACTATTGTAACTGGAGCTGGAGATG
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Plant Biology Division
The Samuel Bolosy Division
The Samuel Boberts Noble Foundation
Tel: 580 221 7391
Fax: 580 221 7380
Faxi: 580 221 7380
Insert Length: 630 5td Error: 0.00
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                                                                                                                                                                                                                                                                                                                         Score 620.6; DB 12; Length 630;
Pred. No. 4.4e-72;
0; Mismatches 7; Indels 0;
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Direct Submission
Submitted (12-ApR-2002) Maize Mapping Project, University of
Submitted (12-ApR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
wearching at MSL, maizemap.org; ZmDB, www.zmdb.isatate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. . . . . (bases I to 1633)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
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                                                   181 AGATCTGCTTCGAAATTCGCTTTGTTTGATATCAATACTCCGACGGAAGAAGACGCGATGAT
                                                                                                                                                                                                                                                     301 CCGGTTACGCCCGGAGAAACGACTCGCCGTCGATGACATTGCCGAATAGATATTTTT
                                                                                                                                                                                                                                                                                                                                                361 AGGTATAAGACGGAGACGAGACAGTCCATGCACTCGCTTTCGCCGTTTATGGATGATGAT
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                                                                                                                                                                                                                                                                                                            530 AGGIATAAGACGAGACGAGACAGICCAIGCACICGCITITCGCCGTITAIGGAIGAI
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                       <u> AGATCTGCTTCGAAATTCGCTTTGTTTGATATCAATACTCCGACAGAAGGACGCGATGAT</u>
                                                                                                                 AGTICCAGCGCITATACGACTCTTCTGAGAACGCCGTTGTTTGGACCGGATGTTGCCGGT
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/mol_type="mRNA"
/db_xref="MaizeDB:631015"
/db_xref="taxon:4577"
/clone lib="Maize Mapping Project/DuPont Cornsensus Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTCACACAATGTTGGCTGTTGGTTTGGGTAACTGTGTCTATCTCTGGAAT 763
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/tissue_rvogaveru-
/tissue_rvoge="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."
/clone_lib="Developing flower"
/clone_lib="Developing flower"
/note="Wector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods The CDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinant Uni-ZAP XR vector
using ExAssist helper phage and the E. coli strain
XII-Blue MRR* (Stratagene). Excised plasmids were plated
using SOLR cells."
                                                                                                                                                                                                                                                             Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids
, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 594)

Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
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NF069G04FLIF1036 Developing flower Medicago truncatula cDNA clone
NF069G04FL 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: 9dmay@noble.org
Insert Length: 594 Std Brror: 0.00
Plate: 069 row; G column: 04
Seg primer: TCACACAGABAACAGTATGAC.
Location/Qualifiers
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|mol_trype="mRNA"
|db_xref="taxon:3880"
|clone="NP069G04FL"
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/lab host="Monte securing, 2 week Old, elloated / Lab host="Monte securing, 2 week Old, elloated / Lab host="Monte libe"Gm-c1059"
/clone libe"Gm-c1059"
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/clone libe"Gm-c1059"
/clone libe"Gm-c1059"
/clone libe"Gm-c1050 in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stripe in Stri
                                                                                                                      648 bp mRNA linear EST 28-NOV-2001 saa35d02.yl Gm-c1059 Glycine max cDNA clone GENOMB SYSTEMS CLONE ID: Gm-c1059-939 5' similar to TR:Q9XED5 Q9XED5 CELL CYCLE SWITCH BG044933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemsker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Martan, H., Hillier, L., Kucaba, T., Martin, J., Beck, C., Awylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       information
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae;
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Public. Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Bmail: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further informa
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 GGAACTAACAATGGTAAAGTTCAGATTTGGGATGCAAGATGCAAGAAGATAAGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mkN4"
| db_xref="texon:3847"
|clone="CENOWE SYSTEMS CLONE ID: Gm-c1059-939"
| /tissue_type="Whole seedling, 2 week old, etiolated"
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Pred. No. 5.2e-62;
0; Mismatches 65; Indels 0;
AGGAACATCTTTCGTTAGAAGCTACATCCGGTGA 1024
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al Similarity 90.0%;
582; Conservative
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Glycine max
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Best Local S
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                        TGATTTTTTATCTGAATCTGGTAGATTGGTCTTCACACAATGTGTTGGCTGTTGGTTTGGG
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                                                                                                                Length
                                                                                                                                                                        Indels
                                111
                                                                                                                   11;
                                                                                                                Score 571.8; DB 11;
Pred. No. 5.7e-66;
); Mismatches 264;
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ilarity 72.8%;
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AW980816 S58 bp mRNA linear BST 07-SEP-2000 EST391969 GVN Medicago truncatula cDNA clone pGVN-58F10, mRNA sequence. AW980816
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                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGGAACTAGCAATGGGAAAGTCCAAATTTGGGATGCATCTCGTTGTAGAAGGATAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1037 AGTAAACTGTCAGGACACAAATCAGAGGTTTGTGGACTGAAGTGGTCATATGATAACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIICAIGGACIICIIGIAICIAGGGGGAGGAACIGCAGACGGGGGACGGGGTICGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1277 ACAACCACAAACTCACACCTTAGCTGTATGGACACTGGAAGTCAGGTTTGCAATCTTGTC
                                                                                                                                       sequence analysis go to
http://www.genome.cleamson.edu/projects/peach. To order
http://www.genome.clemson.edu/orders"
this clone go to http://www.genome.clemson.edu/orders"
this clone go to http://www.genome.clemson.edu/orders"
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         /lab_host="E. coli" - r /lab_host="E. coli" - r /lab_host="E. coli" - r /lab_host="Peach developing fruit mesocarp" ECORI; note="Vector: pBluescript II SK(-); Site_1: ECORI; Site_2: XhoI; authority=Prunus persica L. Batsh; The sequence has been trimmed to remove vector sequence a contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                13; Length 677;
                                                                                                                                                                                                                                                Score 499.4; DB 13; Length
Pred. No. 3.1e-56;
0; Mismatches 104; Indels
tissue_type="Mesocarp"
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Best Local Similarity 84.5%;
Matches 571; Conservative
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BU042571.
BU042571.1 GI:22482648
BST.
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1 (bases 1 to 677)
Callahan,A., Palmer,M., Main,D., Wing,R. and Abbott,A.
Peach Model Genome for Rosaceae
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                                                                                                                                                                                TTGGCATCTGGAGGAAATGACAAATTGTTTGTTTTGGAATCAACACTCAACCCAGCCT
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ATGGAGGGTCATCGGTTACGGGTTGGGCCTTGGAGTTCATCTCTTTTGTCTTCT
                                    GGTGGACGGGATAAGAATATTTATCAACGAGATATACGCACACAAGAAGATTTTGTTAGT
                                                          1460 TATCTTGCCATCTCTCCAGATGGACAGACTATTGTAACTGGAGCTGG 1506
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Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC
Tel: 864 656 3060
Fax: 864 656 6879
Email: aalbertgeclemson.edu
Total High Quality bases = 577
Seg primer: TAATACGACTCACTATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..677
/organism="Prunus persica"
/nol_type="mRNA"
/cultivar="Loring"
/db_xref="taxon:3760"
/clone="PP_LEa0013C06f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 677.
Location/Qualifiers
                                                                                                            1040 AAACTGTCAGGACACAAATCAGAGGTT
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Prunus persica
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JOURNAL
COMMENT
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Gaps

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481

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Gossyptum arboreum Eukaryothyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids Spermatophyta; Malvaceae; Malvaceae; Gossypium.

1 (bases 1 to 987)

Wing, R.A., Prisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                               1679
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/db xref="taxon:29729"
/clone="dA_E80023N11f"
tissue_type="Pibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
203 c 256 g 265 t 5 others
                                                                                                                                                 CATTGCAGCCTAATCATGTGGCATATTTCTAAGATTGGAGAGATAGCTAGAACTAAATTTA
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                                                                   301 creaaagreaarceeagcarrarcrerresaagaacracrarcagrearresagrearceres
                                                                                                                     1620 CGTTGCAGCCCAATCATGTGGCATATTTCTAAGTTTGGGTTGCTGTGTAGAACTAAATTT
                                                                                                                                                                                                                  1680 CTGAGCGGAGAACACCATGGTGGAAAAACCTTGAATATAAAAACACCACCAAAGTAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wing RA
Clemson University Genomics Institute
Clemson University
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 987
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence start: 40
High quality sequence scop: 800.
Location/Qualifiers
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/lab host="E. coli"
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Matches 550; Conservative
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BG444274
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/organism="Medicago truncatula"
/organism="Medicago truncatula"
/oultivar=genotype A17"
/dlivar=genotype A17"
/dlisue_type="Medicago"
/dlone="pgWw-58F10"
/tlsue_type="effective root nodules harvested one month gost_inoculation with Sinorhizobium meliloti"
/tlone lib=not="E. coli strain XLOLR"
/dlone lib=ngwm
/dlone lib=ngwm
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Giapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: vance004@maroon.tc.umn.edu
University of Minnesota name:M256650e
TIGR sequence name:WTCBR29TK
More information is available at. . http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                               Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
11 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                Fedorova, M., Fierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Pe, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M. ESTS from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1320 AGGTTTGCAATCTTGTCTGGTCCAAAAATGTCAACGAACTAGTAAGCACACATGGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AGGITTGCAATCTTGTCTGGTCCAAAATGTGGATGAACTAGTAAGCACACATGGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1380 CCCAGAACCAGATTATTGTTTGGAGATACCCCACTATGTCAAAGCTGGCGACTCTTACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.260 GTATTCGTTTTTGGAATACAACCACAAACTCACACCTTAGCTGTATGGACACTGGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTATTCGTTTGGGAATACAACCACAAACTCACACCTAAGCTGTATGGACACTGGAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTGGAGATGAAACGCTTAGGTTCTGGAATGTTT
                                            Medicago truncatula (barrel medic)
Medicago truncatula
  AW980816.1 GI:8172357
                                                                                                                                                                    Medicago.
1 (bases 1 to 558)
                                                                                                                                                                                                                                                                                                                        truncatula
Unpublished
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Matches 514;
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Best Local (
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CA837263

MCT003C07 164457 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT003C07 5, CA837263. GI:26565028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGGACAGACTATTGTAACTGGAGCTGGAGATGAAACGCTTAGGTTCTGGAATGTTTTC 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bapermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 680)
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                                                                                                                                                                                                                             /note="Organ: Nodule; Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; The library was prepared using mRNA extracted from nodules of 5 and 7 week-old Lotus plants. Nodules were induced by, and contained Mesorhizobium strain R7A."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAGTAAGCACACATGGGTACTCCCAGAACCAGATTATTGTTTGGAGATACCCCCACTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 528;
1. .528
/organism="Lotus japonicus"
/moltype="mmNA"
/cultivar="difu" (B-129)"
/db_xref="taxon:34305"
/db_yeage="5 and 7 week-old plants"
/clone lib="Lotus japonicus nodule library
week-old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTCCCCTAAATCAGAATACTGAAAGTGAAATCGGAGCA 1579
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Pred. No. 1.9e-51;
0; Mismatches 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.1%;
Best Local Similarity 92.9%;
Matches 485; Conservative
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CB828401
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Lotus japonicus
Lictus japonicus
Eukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosidi,
eurosida I; Fabales, Fabaceae, Papilionoideae, Loteae, Lotus.
(Dases I to 528)
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTE: tools for functional genomics
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509
                                                                                                                                                                                                                                                269
                                                                                                                                                                                                                                                                                                                                                                    329
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            GGGTGAGGGCCTTATCTTGGAGCTCTTCTCTGTTATCTTCTGGTAGTCGTGATAAGAGCA 149
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                                                                                                                           rrcrrcaaagagararacegagaagargarririgeragraaacrercregercaaagr
                                                                                                                                                                                       CAGAGGTTTGTGGACTGAAGTGGTCATATGATAACCGTGAGTTGGCATCTGGAGGAAATG
                                                                                                                                                                                                                      210 CAGAGGTTTGTGGGCTGAAGTGGTCTTATGACAACCGGGAGCTAGCATCTGGCGGAAATG
                                                                                                                                                                                                                                                                                                            ACAACAAATTGTTTTGGAATCAACACTCAACCCAGCCTGTCCTCAAGTACTGTGAGC
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                                                                           TITATCAACGAGATATACGCACACAAGAAGATTTTGTTAGTAAACTGTCAGGACACAAAT
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Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
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High quality sequence stop: 528.
Location/Qualifiers
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0SJNEellC18.f OSJNEe Oryza sativa (japonica cultivar-group) CDNA clone OSJNEellC18 5', mRNA sequence.
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                                           1524
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                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhattoideae; Oryzeae; Oryza
1 (bases 1 to 856)
Jantaeuriyaratı, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
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                                                                        502 ATAGCCTAGCATGTCAAAGTTGGCAACTCTTACAGGACACACTTACAGAGTTCTTTATCT
                                             1465 IGCCATCTCCAGATGGACAGACTATTGTAACTGGAGCTGGAGATGAAACGCTTAGGTT
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/organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                            CIGGAAIGITITCCCTIAAAICACAGAAIACIGAAAGIGAAAICGGA 1576
                                                                                                                                                   622 CTGGAATGTCTTCCCTTCTCCAGTCTCAGAACACTGATAGCGAGCTCGGA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, 85721-0088, USA
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Pred. No. 3.2e-44;
0; Mismatches 160; Indels
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: C column: 18
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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cultivar="mgNA"
db xref="taxon:39947"
clone="0SJNEe11C18"
fissue_type="leaf"
dev_tatage="a" week"
|lab host="pill:0B"
|clone="lib="CSJNEe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: http://genome.arizona.edu
PCR PRimers
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Best Local Similarity 75.99
Watches 503; Conservative
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Fax: 520 621 9288
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/db_xref="taxon:3544"
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/tissue_type="leaf"
/clone="McT03007"
/tissue_type="leaf"
/clone=lib="Ico plant Lambda Uni-Zap XR expression library
/clone=lib="Ico plant Lambda Uni-Zap XR expression library
/clone=lib="Ico plant Lambda Uni-Zap XR expression library
/clone=lib=rice plant Lambda Uni-Zap XR expression library
/sdays 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase IV (5:30 PM)."
/note="wector: Lambda Uni-Zap XR pectors"
EcoRI: Site_1: Lambda UniZapXR vector; and cDNA synthesis kit."
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                           database for the common ice plant,
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                                                                                                                                                                                                                                                                                                                                                    680.
                                                                                                                                                        USA
                                                                                    Contract: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USP
Tel: 775-784-1918
Fax: 775-784-1650
Email: joushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T7 21mer
BACKWARD: T3 20mer
Flate: 003 row: C column: 07
Seq primer: T3 20mer
High quality sequence atop: 686
High quality sequence
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                        An expressed sequence tag data
Mesembryanthemum crystallinum
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           Cushman, J.C.
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Alcala, I amiles; Solanales; Solanaceae; Solanum; Lycopersicon.

Loases 1 to 710)
Alcala, J., Yebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato callus tissue
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TAMU Lycopersicon esculentum cDNA clone
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314 ATTGGGGAATTGTGTTTATGGAATGCATGCAGCAACAAGGTCACCAAGCTATGTGA
                                                                                                                          434 richadgakchahcchadgachhadritchreinnidgdahdccacrcdhighadadahhhad
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                                                                                                                                                         ATCAATGGAGGGCCATCGGTTACGTGGGGGCCTTGGCCTGGAGTTCATCTTTTGTC
                                                                                                                                                                                          494 AACCATGGAAAGCCATCGGATGCGAGTAGGTGCTCTTGCATGGAATTCATCATTGCTTTC
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lycopersicon esculentum"
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/mol_type="manna"
/db_xref="taxon:4081"
/db_xref="taxon:4081"
/clone="clac55823"
/tissue_type="callus"
/dev_stage="25-40 days old"
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/note="vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses: Tomato Callus EST Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1446 CTTATAGGGTTCTCTATCTTGCCATCTCCCAGATGGACAGACTATTGTAACTGGAGCTG
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1 (Dases 1 to 460)
Pirnhaber,C., Bartelsmeier,V., Meyer,F., Bartels,D., Bekel,T.,
Linke,B., Puehler,A. and Kuester,H.
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19.5%; Score 392; DB 9; Length 71
Best Local Similarity 79.5%; Pred. No. 3.4e-42;
Matches 464; Conservative 0; Mismatches 120; Indels
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/lab_host="XL1-Blue MRF'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by S. Rudd of the (http://mips.gsf.de
                    Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Varidiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Embrartoidaes; Oryzeae; Oryza.
1 (bases 1 to 909)
Bennett,J., Arumugam,K., Lafitte,R., Wen,J., Rudd,S. and
Enskiewich,R.M.
IRRI Drought Stress Panicle cDNA Library
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    .909
        (cryanism="Oryza sativa (indica cultivar-group)" (mol.type="mRNA" (cultivar="IR64")

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +63.2-845-0606
Email: r.bruskiewich@cgiar.org
International Rice Information System (IRIS;
http://www.iris.irri.org): D0200596
Assignment of putative function to the sequence land information Center for Protein Sequences
                                                                                                                                                                                                                                                                                                  replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.0%; Score 342; DB 14;
80.1%; Pred. No. 1e-35;
ative 0; Mismatches 100;
                                                                                                                                                                                                                                                                                      On Dec 2, 2002 this sequence version in Contact: Richard Bruskiewich Biometrics and Bioinformatics Unit International Rice Research Institute DAPO 7777, Metro Manila, Philippines Tel: +63-2-845-0563
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Location/Qualifiers
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Best Local Similarity 80.1
Matches 402; Conservative
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                                                                                                                                                                                                                                          /organism="Medicago truncatula"
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from developing pods including seeds harvested at
different stages of development. The cDNA was
directionally ligated by Medicenomix into the pGEM-T
vector from Promega using GCATGCGGCCGACGGCGACATG and
cTGCAGGCCATATGGCCGGA dappers. Plasmids containing cDNA
inserts were propagated in E. coli DH10B cells."
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AF53-Rpf 02 I21 T7 085.abl IRRI Drought Stress Paniacle Library Oryza sativa (indica cultivar-group) cDNA closs C0000597 5: similar PMC1-ITG2 intergenic region, mRNA sequence.

CA764180.2 GI:27545893
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Location/Qualifiers
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Db 362 ACATTGACGACCATACATATAGGTATTATATTTAGCCATCTCCCCAGATGGACAGACT 421

Qy 1490 ATTGTAACTGGAGGTGGAGATGAAACGCTTAGGTTCTGGAATGTTTCCCTTCCCCTAAA 1549

Db 422 ATAGTAACTGGTGATGAAACGCTTCGGTTTTGGAACGTGTTTCCATCTCCCAAG 481

Qy 1550 TCACAGAATACTGAAAGTGAAA 1571

Db 482 TCCCAGAGTTCTGACAGACAAA 503
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Search completed: January 23, 2004, 21:05:55 Job time : 4362 secs